SVR was more frequent in women than in men (43/63, 62.8% vs. 62/116, 53.4%) ($P = 0.059$).

Conclusion: 1) Negative serum HCV RNA at week 12 is more predictive of SVR than EVR. 2) The probability of SVR was significantly higher in patients with lower baseline viremia, body weight and younger adults. 3) Gender was not significant for the efficacy of treatment.

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67.017

Prevalence of Hepatitis C Virus (HCV) Genotype 3a in the Infected Population of Lahore, Pakistan

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Keywords: Hepatitis C virus; Genotype 3a; PCR; Lahore

Hepatitis C virus (HCV) major public health concerns in Pakistan. A molecular study was conducted to investigate the prevalence of Hepatitis C Genotype 3a in the infected population of Metropolitan. By using primers against the 5′ non coding region of the viral RNA was reverse transcribed into cDNA and for qualitative analysis, the amplification of cDNA was done by first round PCR. Nested PCR was performed with first round PCR product. Amplification of HCV cDNA for genotyping by regular PCR was carried out. For HCV genotyping second round PCR, two different primer mixtures were prepared. Detection of genotype specific band was performed through gel electrophoresis. 232 bp specific band of HCV 3a genotype was determined by comparing with 100 bp DNA size of marker. Our result showed, out of 28 HCV PCR positive samples, fifteen samples have HCV genotype 3a. The prevalence of genotype 3a HCV RNA was found to be 55% in local population of Lahore.

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Diagnosis Dilemma of Chronic Hepatitis

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One of the most frequent reasons of hepatitis is HCV virus infection. There are two methods of infection detection: immunological and genetic ones.

The study was made on 361 patients with the features of liver pathology admitted to the Clinic during the years of 2000—2004. Besides standard methods aimed to determine disease aetiology and the level of liver damage, the blood serum tests were made simultaneously. There were as follows: detection of anti-HCV antibodies by the quality Cobas Amplicor 2.0 test. The tested population underwent outpatient observation for at least six months.

The anti-HCV antibodies were detected among 256 patients, RNA-virus was detected among 212 patients. The results of both of these tests were negative for 102 patients and positive for 209 patients. The RNA-virus was not detected among 47 patients with presence of the anti-HCV antibodies. The RNA-virus was detected for three patients without presence of the anti-HCV antibodies. The following observation and performing the tests such as liver biopsy led to diagnose hepatitis virus infection among all the patients with detected at least single infection marker. Four patients were diagnosed as the acute infection cases and 255 as chronic infection cases. The following next months' observation did not led to detect any changes for the infection status of patients without infection markers.

The detection of the anti-HCV antibodies in the blood serum with the third-generation tests should be treated as the standard procedure in the liver infection diagnosis.

The detection of HCV RNA can be reasonable in the following cases: suspected acute HCV infection, unclear clinical picture; particularly when the possibility of infection related claims occur, drug addicts and patients suspected for taking drugs, review of antiviral therapy effectiveness.

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Hepatitis B Virus in Chronically Infected Patients

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Background: Genomic mutations presented during hepatitis B virus (HBV) reverse transcription could explain its genetic diversity and account for genetically distinct eight genotypes which show distinctive geographically distribution. The main objectives of this study were to determinate the prevalence of hepatitis B virus genotypes in patients with chronic hepatitis B, and to look for a relationship between genotypes and risk transmission factors according to HBeAg state.

Patients and methods: A total of 14 serum samples from chronic HBV patients were analysed using INNO-LIPA HBV Genotyping assay (Innogenetics). The presence of mixed genotype infection was verified by sequencing using the BigDye Terminator Cycle Sequencing Kit on an ABI Prism 3130 Genetic Analyzer. Hepatitis B virus HBsAg, anti-HBs, HBeAg and anti-HBe were determined by ADVIA Centaur (Bayer).

Results: Genotype D was the most prevalent (64.3%) followed by genotype A (28.6%). There was a coinfection case (D/E genotypes) that was confirmed by sequencing PCR